


```

0Y 331 -ESVNLEGGDVIIRIPAGTFYFLIRKONNRRHLIAKFLQITSTGGQXKEFPBAGQUNPEY 389
    | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 473 KESYVEGGDWITIPAGTITVLAAQ--NEDLQIVKLQVPPANNBERKDYIUSAGES--QA 530
    | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
0Y 390 LSTFKEELLEALMTQTEKLGVGQOORE-GVIRASQEOIRELTFPDDSESRHHIIRG 447
    | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 531 YSFSNDVLEAALNIPDKLEIRITKÖRREKGGKIVRASQDLALSO-----RATSYRKG 585
    | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
0Y 448 GESSKCPNLFNKRPLYSNKYQAEVKEKPEDYROLQMDLSVEFIANTQGSMMGPFFNTR 507
    | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 586 SRGVNAPITKLESQPPVYNNQYGGQFEACPDPEPQLRTDVAITSVVIDKQGGMVVPHFNKR 645
    | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
0Y 508 STKVYVVASGADYEMACPHILSGRHGGRGGK----RHEEED----VHYDQVBARUS 557
    | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 646 ATWVYVEGAGSEFMACPHIOSOMQGRREERBEHRREEBERBERSGRFEFVARGURS 705
    | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
0Y 558 KREALIVLAGHPVYVSSGNENLLFAPFIMAQNHNENFLAGERNVLOIEQANELAF 617
    | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 706 EGGVIVIPAGHPILIMASPNENLTVGFGINAENNRHNFLAGRE-NIMNELDEAKELAF 764
    | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
0Y 618 AAPRKEVESFNQDOSIFFFGCPRHQHQOSPRSKQQQQLVSLTDPVGF 666
    | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 765 NVEGQAOEIRFSQRESFTEGP---EGGRRRSTESPLIILTKLAGY 809
    | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

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RESULT 2

S22477
vicillin precursor - cacao

C:Species: Theobroma cacao (cacao)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999
C:Accession: S22477; S22478; S18105; S22050
R:McHenry, L.; Ertz, P.J
Plant Mol. Biol. 18, 1173-1176, 1992

A:title: Comparison of the structure and nucleotide sequence of vicillin genes of cocoa
A:Reference number: S22477; MUID:92288309
A:Accession: S22477

A:Molecule type: DNA
A:Residues: 1-566 <MCH>
A:Cross-references: EMBL:X62625

A:Accession: S22478
A:Molecule type: mRNA
A:Residues: 1-452 <MC2>
A:Cross-references: EMBL:X62626

C:Genetics:
A:Introns: 211/1; 269/3; 296/3; 391/3; 502/1
C:Superfamily: seed; storage protein
C:Keywords: seed; signal sequence #status predicted <SIG>
F:1-24/Domains: signal sequence #status predicted <MAT>
F:25-566/Product: vicillin #status predicted <MAT>

[illegible][illegible]

RESULT 3
S06398
alpha-globulin type A precursor - upland cotton
N:Alternate names: seed storage protein
C:Species: *Gossypium hirsutum* (upland cotton)
C:Date: 31-Mar-1990 #sequence revision 31-Mar-1990 #text change 30-Sep-1993
C:Accession: S06398
R:Chan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L.
Plant Mol. Biol. 9, 533-546, 1987
A:Title: Developmental biochemistry of cottonseed embryogenesis and germination. XIX
A:Reference number: S06398
A:Accession: S06398
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-605 <CHL>
A:Superfamily: glycinin
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-605/Product: alpha-globulin type A #status predicted <MAT>

Query Match	30.8%	Score 1092;	DB 2;	Length 605;
Best Local Similarity	36.4%	Pred. No. 4.3e-61;		
Matches 250;	Conservative 117;	Mismatches 210;	Indels 110;	Gaps 17;
QY	1	MAINTNSLCISLFLSTLSTFLSTTYSLAE-----SEFPD-ROEYEECKRCQMOLETSQOMR	53	
Db	1	MYRNKSVFVLLF--SLFSLFGLLSANDPGRSRBEDPQGYEDCKRKN-OLETRGQTE	57	
QY	54	RCVSGCDKRFEEIDMSVYDNODEDQTEQCCQCRRCROOESPRQOYQCDQRKCEICEE	113	
Db	58	Q--DICEPDRSETQLNEEDQRODGEDPQRRYQDGRHCQOEDERLP-----HCEOSCRQD	109	
QY	114	EEYNRQDPQOQYEQGCKHCQRFETEPRHMCQOORCEERYKEKKRQOKRYEQQREDE	173	
Db	110	YEKQOQOQDPDKQFKCCQRCQOMQOEORPERKQOCYACECBQYOEDEWKBGR-----E	160	
QY	174	EKEYERMKDEEDKRPQDQREYEDCRRRCEQEQRQDHQCSLRCQEQROHNGRGDMMNPQ	233	
Db	161	NKWRREEEES-----	171	
QY	234	RGSGSRYEEGEEQSDNYEFEDERSLSTRFTEEGHISVLENFYGSKLRLALKNYRLV	293	
Db	172	-----DEGEQOQNNNYTFHRSFQERFREBEHGNFRLOYFADKHHLLKGINFRFAI	224	
QY	294	LEANNAFVLPHTLDADAILLVIGSGALAKMTHHGNRESYNLECGDVRIRIPAGTFYPLN	353	
Db	225	LEANNTVFLPHHCDAEKIITYVTNRGIVTFVTHHNKSKSYNVPQVYVIRIPAGSTVYLAN	284	
QY	354	RDNNERLIARFLQISTIPGOYKEEFPFAGGONPEPYLSTFSKEILMALINTOTEXLRGVF	413	

[illegible]

RESULT 4
FWCNCAB
alpha-globulin B precursor (clone C72) - upland cotton
N:Alternate names: seed storage protein; vicilin precursor
C:Species: *Gossypium hirsutum* (upland cotton)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C:Accession: A30836; 506911
R:Chlan, C.A.; Pyle, J.B.; Legocki, A.B.; Dure III, L.
Plant Mol. Biol. 7, 475-489, 1986
A:Title: Developmental biochemistry of cottonseed embryogenesis and germination XVIII CLE
A:Reference number: A30838
A:Accession: A30838
A:Molecule type: mRNA
A:Residues: 1-588 <CH>
A:Cross-references: GH:M16891; NID:g167374; PIDN:AA33071.1; PID:g167375
A:Experimental source: var. Coker 201
R:Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L.
Plant Mol. Biol. 9, 533-546, 1987
A:Title: Developmental biochemistry of cottonseed embryogenesis and germination. XIX. Seed
A:Reference number: S06398
A:Accession: S06911
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-81 <CH2>
C:Comment: This is a seed storage protein.
C:Superfamily: glycinin
C:Keywords: glycoprotein; seed; storage protein
F:1-25/Domains: signal sequence #status predicted <SIG>
F:26-588/Product: alpha-globulin storage proprotein #status predicted <MAT>
F:7417/Binding site: carbohydrate (Asn) (covalent) #status predicted

[illegible][illegible]

RESULT 5
S08059
alpha-globulin type B precursor (tandem 1) - upland cotton (fragment)
N:Alternate names: seed storage protein
C:Species: *Gossypium hirsutum* (upland cotton)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 30-Sep-1993
C:Accession: S08059
R:Chan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L.
Plant Mol. Biol. 9, 533-546, 1987
A:Title: Developmental biochemistry of cottonseed embryogenesis and germination. XIX
A:Reference number: S06398
A:Accession: S08059
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-509 <CHL>
C:Superfamily: glycinin

[illegible]

[illegible]

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RESULT      6
A53234
globulin-1S, GIB1S - maize
C:Species: Zea mays (maize)
C:Date: 02-May-1994 #sequence-revision 18-Nov-1994 #text-change 11-Jan-2000
C:Accession: A53234; A43642
R:Belanger, F.C.; Kriz, A.L.
Genetics 129, 863-872, 1991
A:Title: Molecular basis for allelic polymorphism of the maize Globulin-1 gene.
A:Reference number: A53234; MUID:92090707
A:Accession: A53234
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-573 <BEL>
A:Experimental source: Inbred line Va 26
A:Note: sequence extracted from NCBI backbone (NCBIN:71280, NCBIPI:71284)
R:Kriz, A.L.
Biochem. Genet. 27, 239-251, 1989
A:Title: Characterization of embryo globulins encoded by the maize G1b genes.
A:Reference number: A43642; MUID:89374022
A:Accession: A43642
A:Status: preliminary
A:Molecule type: protein
A:Residues: 87-100 <KRI>
A:Superfamily: glycinin

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Query Match	25.6%	Score	908;	DB 2;	Length	573;			
Best Local Similarity	39.9%	Pred.	No. 1.3e-49;						
Matches	201;	Conservative	91;	Mismatches	180;	Indels	32;	Gaps	10;

QY	182	EDDKRDPQOREYDGCRRRCEDOEPRROHCOOLCRRCQOHQRCGMMN-PQGGSG--	238
Db	25	EDDHHHHHHGHSKRCYVRKREDPRWHORPRLCQREEREKQERSRHEADRSGGSS	84
QY	239	-----RYEEGEESQD-NPYYFDESLSTRFRTTEGHISYLENFYGSKLRLAKNRLV	292
Db	85	EDERERQKEBEKQKDRPYPVDFRRSRVRRVREESGLRLRFREDESLRLRLRQYRA	144
QY	293	LEENPNAFVLPTHLDAAILLVYIGRGALKMTIHHNDRSEYNLECGDYIRIPAGTFYLI	352
Db	145	VLEANPRSPFVPSHTDHAHCICYAECGCVYTTIENGERRSYTIKQGHVFAVAGAVTYLA	204
QY	353	NRDNNEHLHAKELQTTISTPGQYKKEFPAGCONDEPLSTFSKELLEALINTQTEKRGV	412
Db	205	NTGGRRKLLVTKLILHTISVYGEQFFEGPGRGNREPLSTFSKSIORAAKTTSSDRLERL	264
QY	413	FGQ--QHEGVIIASQOQITHELTRDSE---SKHHMIRRGEGSSRGRYNLFNKRPLYSNK	467
Db	265	FGRRGQDGLIVATEQOTRELRHRHASEGHCGRWPLPRPGE-SRGPYSLIDRPSIAND	323
QY	468	YGAQAEVKRPEDYQLOLMDMLSVFLANTQGSMMGPREFNSTKVVVVYASGEADENWACPH	527
Db	324	HGQIYTEADARSFHLDAHDVSVSFANTTASMSAPRLYNTSFIAVVPCKGAEIYVCPH	383

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OY 528 LSGRNG-----GGGGKHNHEEDVDHYQO-----VRARLSKREAIVYLACHPVVFS 574
Db 384 ROSGGGSESERERGGKRSRSEEESESEBOEGVGYHTIRARLSPTGAFFVPAAPHAPVAA 443
OY 575 SGENULLLFAGIAQNNHNHEFLAGRENVLOOIEPQAMLEAFAPRKEVEESFNQDS 634
Db 444 SRDSLOLVCEVYHADNRKEKFLAGAG-NVLOKIDRYAKALSFAASKAAEVEDVLGRREK 502
OY 635 IFPGPPO---HQQQSPRSTKQOQ 655
Db 503 GFLPGPKBSGGHREEOEEEREE 526

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RESULT 7
B53234
vicilin-like storage protein glob1-L, embryo - maize
N:Alternate names: globulin-1L
C:Species: Zea mays (maize)
C:Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
C:Accession: B53234; S21824
R:Belanger, F.C.; Kriz, A.L.
G:Genetics 129, 863-872, 1991
A:Title: Molecular basis for allelic polymorphism of the maize Globulin-1 gene.
A:Reference number: A53234; MUID:92090707
A:Accession: B53234
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-582 <BEL>
A:Cross-references: EMBL:X59083; NID:g22283; PIDN:CAA41809.1; PID:g22284
A:Experimental source: Inbred line W64A6
A>Note: Sequence extracted from NCBI W64done (NCBI:71285)
C:Genetics:
A:Gene: Glob1-L
A:Introns: 167/1; 225/3; 252/3; 349/3
A:Superfamily: glycinin

Query Match	25.48;	Score 898;	DB 2;	Length 582;
Best Local Similarity	39.28;	Pred. No. 5.8e-49;		
Matches 197; Conservative	91;	Mismatches 184;	Indels 30;	Gaps 9

QY	182	EEDKKROQAEYEDCRKRCSDOERPOOHOSOLACREDOQHONGGIMN-PORGSG--	238
Db	25	EDDDNNHHNGHKGSGQCVKRCEDRDMWHDPRCLCECREEERKREKERSRNEADRSGESS	84
QY	239	--RYEEGEEOSONPYYFDERSJSTRFRTEEGHIIIVLENDEYGSKLRLKLVNRLVLE	295
Db	85	EDEKGEKEKCKDKRRPYVFDKRSFRVVRVRSQGLSLKVLRFPPDEVSRLLRIGIRDTYAVLE	144
QY	296	ANPAFVLPYHLDAIDLILYIGFGALKMIHHONRESYNLECGDVIIRIPACTTFFYLNRD	355
Db	145	ANPSPFVVPSTHDDHCICUYAEGGVVTTIENGERRSYTTKOGHVFAPAGAVTYLNTD	204
QY	356	NNEKLIHAKFLQTSITSPGQXKEFPAGGONDEPLTFSFEKLEALANTQOTEKLRGFGO	415
Db	205	GKKLVITKLILHTISVGEQEFQFFGPGCRPRESTLSFSSISQRAAKTISDRLERLPGR	264
QY	416	--QREGVITRASQOIRBELTRDSE--SRHHIRRGESSRGDPYNLKNRPLYSNKYGQ	470
Db	265	HGQDKGILVRATEBOTRELRHNASGEGCHGNWPLRPPEG-SRGQYSLDROPIANOHCQ	323
QY	471	AYEKKPREDYQLOMDLSVFIANTQGSMMGRPNFTSGTVVVVAVASGEADVEMACRYLSC	530
Db	324	LYEDARSFIDLADHDVSVSFANTITASSMSNAPLENTSFKIATVPYPNKGIAEYLCPHRQS	383
QY	531	RHG-----GRGGGKHHEEEDVH-----YEOVRARLKSREALIVLGNHVVFEVSSG	576
Db	384	QCGESREBKRCGRSEDEEBESSSEGEDEAGQGYHTIARLSPTGALFVPGHGFVAVSR	443
QY	577	NENLLFAFGINAOONHNEMLAGHERVAVLQOIEPOMELAFAPARKVEEVSFNQSDOSTF	636
Db	444	DSNLOIQCFEVHAARNRKVFAGAD-VVLOKLRVAKALFASAEEDVLSRRKCGF	502


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OY 474 VKPEYRLOJMDLSVFLANTQSSMMGPFFNRTSTVVVVVVASGEADVENACHLSGRBC 533
Db 425 ITPENKPOLRDLIDFLSTVDNNEGALLPHFNASKAIVLILINGDANIEV----- 475
OY 534 GRGGK-----RHEEEDVHYEQRARLSKREALVVLGHPVVFSSGNENLLFPAFGIN 588
Db 476 ---GLKEQDQDQDQDEQPLEYKRTKRLSEODITVIFAGTPIVVY--NATSNLFEFAIGIN 530
OY 589 AONNHENFLAGERNNVLQOITEPQAMELAFAPRKVEYESFESNDQSIFFPCPRHOHQSP 648
Db 531 AENNORNFLASQONNVISQIPSOVELAFPGSAQAVELKLNQRESYFVDAQKKKEGN 590
OY 649 RSTQOQPLVSIL 661
Db 591 KGRK--GPLSSIL 601

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RESULT 12

S00566

convicillin precursor (clone pJc4) - garden pea

C:Species: Pisum sativum (garden pea)

C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 20-Aug-1999

C:Accession: S00566

R:Born, D.; Ellis, T.H.N.; Gatehouse, J.A.

Biochem. J. 251, 717-726, 1988

A:Title: The sequence of a gene encoding convicillin from pea (*Pisum sativum* L.) shows th

A:Reference number: S00566; MUID:86326208

A:Accession: S00566

A:Molecule type: DNA

A:Residues: 1-571 <BOW>

A:Cross-references: EMBL:X06398; NID:920698; PIDN:CAA29695.1; PID:q13670

A:Note: part of this sequence, including the amino end of the mature protein, was confir

C:Genetics:

A:Gene: cvcA

A:Map position: 2

A:Introns: 221/1; 279/3; 304/3; 412/3; 507/1

C:Superfamily: glycinin

F:1-38/Domain: signal sequence #status predicted <SIG>

F:29-571/Product: convicillin #status experimental <MAT>

[illegible][illegible]

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RESULT      13
JO1730
62k sucrose-binding protein precursor - soybean
C:Species: Glycine max (soybean)
C:Date: 30-Sep-1993 #sequence,revision 30-Sep-1993 #text_change 26-Aug-1999
C:Accession: JO1730
R:Grimes, H.D.: Overvoorde, P.J.: Ripp, K.: Franceschl, V.R.: Hiltz, W.D.
Plant Cell 4, 1561-1574, 1992
A:Title: A 62-kD sucrose binding protein is expressed and localized in tissues active
A:Reference number: JO1730; MUID:93104680
A:Accession: JO1730
A:Molecule type: mRNA
A:Residues: 1-524 <GR1>
A:Cross-references: GB:L06038; NID:g1431744; PIDN:AAB03894.1; PID:g170064
C:Superfamily: glycinin
C:Keywords: sugar transport
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-524/Product: 62k sucrose-binding protein #status predicted <MAT>

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[illegible]

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Db 317 KRPTISNGCRLTEVGPDDDEKSWLORLMLFTNTITORSMTIYNSHAKIALVIDG 376
OY 518 EADVEMACPHLSGRHGGRGGKHEEEDVHYEQVBARLSKREAIIVLAGHPVYVSSGN 577
Db 377 RGHLOJSCPHMS-----SRSHSHKHDKSSP-SYIRISSDLKPGWVFVYVPPHPTVIASNK 431
OY 578 ENLLFAFGINONHNENFLAGRENVLOQIEPOAMELAFAAPRKEVESEF-----678
Db 432 ENLMLICFEVNAADNKKFTFAGKD-NIVSGLDNVAKELAFNYPSEVNGVFLQREFLERK 490
OY 629 -----NSODSIFFPGRQHQOOSPRS 650
Db 491 LIGRLYHLPHKDKKESFFPELPREGRRA 522

RESULT 14
T06459
62K sucrose-binding protein homolog - garden pea
N:Alternate names: p54 protein
C:Species: Pisum sativum (garden pea)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun-2000
C:Accession: T06459
R:Rodrigo II, M.I.
Submitted to the EMBL Data Library, February 1997
A:Reference number: Z15693
A:Accession: T06459
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-483 <ROD>
A:Cross-references: EMBL:Y11207; PIDN:CAAT72090.1
A:Experimental source: var. Lincoln
C:Genetics:
A:Note: p54
C:Superfamily: glycinin

Query Match 21.7%; Score 769.5; DB 2; Length 483;
Best Local Similarity 31.4%; Pred. No. 5.2e-41;
Matches 162; Conservative 114; Mismatches 169; Indels 71; Gaps 12;

OY 135 RRETERIHMOCTOCRCERYEKKRQKRYEQOQDEDEKYEERMKEDNKRDPQOREY 194
Db 28 RKKDP-ELTTCDCD-----MORQYDEDK-----53
OY 195 EDCRRCEQOEPPOHQOLCRQOQROHGRGDMNPORGSGRYEEGEOSDNPYYF 254
Db 54 RLCMERCDYIKKKQ-----RQKHKEH-----EEDEQOQEDENPYVF 93
OY 255 DERSLSTRTEREGHISYLENFYGRSKLRLAKNRYLVLEAPNAFVLPTHLDADAILL 314
Db 94 EDDPFTKIDTGDGRVLLINKFNEKSKLKNIEYGLAVLEIKANFLLSPHHYDSEAILF 153
OY 315 VIGRGALMIHNDNRESYNLECGDVIRIPAGTFFGLINDNNERLHIKFF--LQTI 371
Db 154 NIKRGITIGLVADRTERRNLEEGDIMRVPAGTPMLVNRDENEKIYIAFHHPSSGSA 213
OY 372 PGQYKEFPFAGGONPEPYLSTESKEILLEALNTQTEKLGVEGQOREGVIIRASQ 431
Db 214 PVNLLEFPFESAGRKPEPVNLTFSSKVLQALAKSSKGELETVLDEQKGRIFKIEK 273
OY 432 LTRDSESKHWHIRRGESSRGPIYLFNKRPLYSNKYGQAYEVKPPDIYQ-LDDML 490
Db 274 LAPKRS--LWPF--GPFKSPFNIFSNPASFNSKFGSLFEVGPQEKSGLEGLNMLT 327
OY 491 IANVQSGSMGPFENRSTRKYVYVVASGEADVEMACPHLSGRHGGRGGKRHEEEDVHYE 550
Db 328 LANITKGSSTHYNTNNAKIALIVDGELELACPHMPS-----SSNSRQKSSISYH 382
OY 551 QVBARLSKREAIIVLAGHPVYVSSGNELLFAFGINONHNENFLAGRENVLOQIEP 610
Db 383 NINAKIRPGVMFYVPRGHPFVNIASKKMLIYVCFEYVNAQRNKKLALAK-KNIV 441
OY 611 QAMELAFAAPRKEVESEFNSODSIFFPGRHQOQ 646
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Db 442 AAKEVAFIAAEKVEDEVFERKEE-FFEPYDNERKE 476
RESULT 15
S24756
vicillin-like storage protein precursor - white spruce
C:Species: Picea glauca (white spruce)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S24756; S18873
R:Newton, C.H.; Flinn, B.S.; Sutton, B.C.S.
Plant Mol. Biol. 20, 315-322, 1992
A:Title: Vicillin-like seed storage proteins in the gymnosperm interior spruce (Picea
A:Reference number: S24756; MUID:93004485
A:Accession: S24756
A:Molecule type: mRNA
A:Residues: 1-448 <NEW>
A:Cross-references: EMBL:X63191; NID:g20500; PIDN:CAA44873.1; PID:g20501
C:Superfamily: vicillin

Query Match 21.2%; Score 752; DB 1; Length 448;
Best Local Similarity 37.8%; Pred. No. 5.9e-40;
Matches 162; Conservative 85; Mismatches 158; Indels 24; Gaps 9;

OY 232 PORGGSGRYEEGEOSDNPYFFDERSLSTRFTEEGHISYLENFYGRSKLRLAKNRYL 291
Db 34 PEYLGRGRGR-EEERENPYVHSDSFTRASSSEAGEIRALPNFGEVSELLEGIRKPY 92
OY 292 VLEAPNAFVLPTHLDADAILLVIGRGALMIHNDNRESYNLECGDVIRIPAGTFFYL 351
Db 93 TCEEMKPNVMLPHYIDATWILVTRGRGLVAVHONELVKRLLEGDVGVPVSGHTFFYL 152
OY 352 INRDNERLHIAKFLQTIOT-PGQYKEFPFAGGONPEPYLSTFSKEILLEALNTQTEK 410
Db 153 VNNDHNTLRISLAVRPVSTVREYOPFYAGGRNQYVSAFSDVLAAPFTNQOLE 212
OY 411 GVFGQOREGVIIRASQOIRELTRDSESRHWHIRRG---GESSR---GPYNLFNKRPL 463
Db 213 RIRGKHSGLVLIHANEQIREMKR-----KRGFSAGSKSADPEHHPFLRNQKDP 262
OY 464 YSNKYQOAEVPRDYRQLODDMLSVFIANYVQSGSMGPFENRSTRKYVYVVASGEADVEM 523
Db 263 FENENGRFTIAGPKNYPFLDALDVSVGLADLPNGSMTAPSLNSKSTSGIVTNGEGRIEM 322
OY 524 ACPHLSGRHGGRGGKRHEEEDVHYEQVBARLSKREAIIVLAGHPVYVSSGNELLF 583
Db 323 ACPHL-GQHG--WSPRERGGDDITYQRYWAKLRIGSYIVPAGHPITELIASNSRLQL 379
OY 584 AFGINONHNENFLAGRENVLOQIEPOAMELAFAAPR-KEVESEFNSODSIFFPGR 642
Db 380 WFDLNRGNEROFLAK-NNVLTITEREIRQLSFNPRGEETEEVLAQKDDVILRG 438
OY 643 HQOQSPRST 651
Db 439 RSRDEARSS 447
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Search completed: March 1, 2001, 15:52:14
Job time: 538 sec